



SEQUENCE LISTING

<110> Guss, Bengt
Nilsson, Martin
Frykberg, Lars
Flock, Jan-Ingmar
Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from
Coagulase-Negative Staphylococcus

<130> guss 09/147405

<140> 09/147405

<141> 1999-04-01

<150> PCT/SE97/10191

<151> 1997-06-18

<150> SE 9602496-3

<151> 1996-06-20

<160> 15

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile
20 25 30

att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca 143
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser
35 40 45

gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca 191
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr
50 55 60

ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag 239
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu
65 70 75

gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act 287

Val	Lys	Glu	Ser	Ser	Ser	Val	Glu	Ser	Ser	Asn	Ser	Ser	Ile	Asp	Thr	
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Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	Ile	Asn	Arg	Glu	Glu	Ser	Val	Gln	
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Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	His	Val	Ser	Asp	Phe	Ala	Asn	Ser	
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Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	Ser	Gly	Lys	Glu	Glu	Asn	Thr	Ile	
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Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	Asp	Ser	Thr	Thr	Ser	Gln	Pro	Ser	
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Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Ala	Arg	Pro	Leu	Ser	Thr	
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Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	Arg	Val	Thr	Val	Asn	Gln	Leu	Ala	
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Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr	Asp	Gln	
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agt	att	act	gaa	gga	tat	gat	gat	agt	gaa	ggg	gtt	att	aaa	gca	cat	719
Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Glu	Gly	Val	Ile	Lys	Ala	His	
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Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp	Asp	Lys	
240					245					250					255	
gtg	aaa	tct	ggg	gat	acg	atg	aca	gtg	gat	ata	gat	aag	aat	aca	gtt	815
Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	Val	Asp	Ile	Asp	Lys	Asn	Thr	Val	
				260					265					270		
cca	tca	gat	tta	acc	gat	agc	ttt	aca	ata	cca	aaa	ata	aaa	gat	aat	863

Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	Thr	Ile	Pro	Lys	Ile	Lys	Asp	Asn		
			275					280					285				
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Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	Thr	Tyr	Asp	Asn	Lys	Asn	Lys	Gln		
		290					295				300						
atc	acc	tat	act	ttt	aca	gat	tat	gta	gat	aag	tat	gaa	aat	att	aaa	959	
Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys		
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gca	cac	ctt	aaa	tta	acg	tca	tac	att	gat	aaa	tca	aag	ggt	cca	aat	1007	
Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn		
320					325				330						335		
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Asn	Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val		
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aat	aaa	aca	att	acg	ggt	gaa	tat	caa	aga	cct	aac	gaa	aat	cgg	act	1103	
Asn	Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr		
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Ala	Asn	Leu	Gln	Ser	Met	Phe	Thr	Asn	Ile	Asp	Thr	Lys	Asn	His	Thr		
		370				375						380					
ggt	gag	caa	acg	att	tat	att	aac	cct	ctt	cgt	tat	tca	gcc	aag	gaa	1199	
Val	Glu	Gln	Thr	Ile	Tyr	Ile	Asn	Pro	Leu	Arg	Tyr	Ser	Ala	Lys	Glu		
	385					390				395							
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Asp	Asp	Ser	Thr	Ile	Ile	Lys	Val	Tyr	Lys	Val	Gly	Asp	Asn	Gln	Asn		
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tta	cca	gat	agt	aac	aga	att	tat	gat	tac	agt	gaa	tat	gaa	gat	gtc	1343	
Leu	Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val		
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aca	aat	gat	gat	tat	gcc	caa	tta	gga	aat	aat	aat	gat	gtg	aat	att	1391	
Thr	Asn	Asp	Asp	Tyr	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile		
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Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys	
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Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr	
480	485 490 495
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc	1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser	
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tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt	1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly	
515	520 525
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa	1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu	
530	535 540
gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg	1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro	
545	550 555
ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa	1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys	
560	565 570 575
tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag	1775
Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln	
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gtc gac	1781
Val Asp	

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 Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu

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Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val		
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Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala		
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Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr		
	100	105
Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys		
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Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu		
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Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly		
145	150	155
Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn		
	165	170
Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr		
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Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala		
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Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser		
	210	215
Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp		
225	230	235
Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val		
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Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro		
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Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser		
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Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile		

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His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn	Asn
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Gln	Thr	Thr	Ile	Asn	Glu	Tyr	Thr	Gly	Glu	Phe	Arg	Thr	Ala	Ser	Tyr
			500					505					510		
Asp	Asn	Thr	Ile	Ala	Phe	Ser	Thr	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Asp
		515					520				525				
Leu	Pro	Pro	Glu	Lys	Thr	Tyr	Lys	Ile	Gly	Asp	Tyr	Val	Trp	Glu	Asp
	530					535					540				
Val	Asp	Lys	Asp	Gly	Ile	Gln	Asn	Thr	Asn	Asp	Asn	Glu	Lys	Pro	Leu

545		550		555		560									
Ser	Asn	Val	Leu	Val	Thr	Leu	Thr	Tyr	Pro	Asp	Gly	Thr	Ser	Lys	Ser
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 gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt ttacaaaag 180
 acccctcaag ataataactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240
 tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300
 gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360
 aaaataaaaag agagtaacac tgaatctggt aaagaagaga atactataga gcaaccta 420
 aaagtaaaaag aagattcaac aacaagtcag cegtctggct atacaaatat agatgaaaaa 480
 atttcaaadc aagatgagtt attaaattta ccaataaatg aatatgaaaa taaggctaga 540
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 gcggaacaag gttcgaatgt taaccattta attaaagtta ctgatcaaag tattactgaa 660
 ggatatgatg atagtgaagg tgttattaaa gcacatgatg ctgaaaactt aatctatgat 720
 gtaacttttg aagtagatga taagggtgaaa tctggtgata cgatgacagt ggatatagat 780
 aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaat aaaagataat 840
 tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900

tttacagatt atgtagataa gtatgaaaat attaaagcac accttaaatt aacgtcatac 960
 attgataaat caaaggttcc aaataataat accaagttag atgtagaata taaaacggcc 1020
 ctttcatcag taaataaaac aattacgggt gaatatcaaa gacctaacga aaatcggact 1080
 gctaaccttc aaagtatggt tacaatatata gatacgaaaa atcatacagt tgagcaaacy 1140
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 ggtgatgaag gttcaacaat tatagacgat agcacaataa ttaaagttta taagggttga 1260
 gataatcaaa atttaccaga tagtaacaga atttatgatt acagtgaata tgaagatgtc 1320
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 <212> PRT
 <213> *Staphylococcus epidermidis*

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 Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr
 35 40 45
 Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp
 50 55 60

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Ser	Ser	Asn	Ser	Ser	Ile	Asp	Thr	Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	85	90	95	
Ile	Asn	Arg	Glu	Glu	Ser	Val	Gln	Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	100	105	110	
His	Val	Ser	Asp	Phe	Ala	Asn	Ser	Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	115	120	125	
Ser	Gly	Lys	Glu	Glu	Asn	Thr	Ile	Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	130	135	140	
Asp	Ser	Thr	Thr	Ser	Gln	Pro	Ser	Gly	Tyr	Thr	Asn	Ile	Asp	Glu	Lys	145	150	155	160
Ile	Ser	Asn	Gln	Asp	Glu	Leu	Leu	Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	165	170	175	
Asn	Lys	Ala	Arg	Pro	Leu	Ser	Thr	Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	180	185	190	
Arg	Val	Thr	Val	Asn	Gln	Leu	Ala	Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	195	200	205	
His	Leu	Ile	Lys	Val	Thr	Asp	Gln	Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	210	215	220	
Ser	Glu	Gly	Val	Ile	Lys	Ala	His	Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	225	230	235	240
Val	Thr	Phe	Glu	Val	Asp	Asp	Lys	Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	245	250	255	
Val	Asp	Ile	Asp	Lys	Asn	Thr	Val	Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	260	265	270	
Thr	Ile	Pro	Lys	Ile	Lys	Asp	Asn	Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	275	280	285	
Thr	Tyr	Asp	Asn	Lys	Asn	Lys	Gln	Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	290	295	300	
Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys	Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	305	310	315	320

Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val Glu
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 Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu Tyr
 340 345 350
 Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe Thr
 355 360 365
 Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn
 370 375 380
 Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn
 385 390 395 400
 Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val
 405 410 415
 Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr
 420 425 430
 Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu
 435 440 445
 Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro
 450 455 460
 Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr
 465 470 475 480
 Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr
 485 490 495
 Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser
 500 505 510
 Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr
 515 520 525
 Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln
 530 535 540
 Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu
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Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala
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Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr
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Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser
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gta caa gac gtt aaa gat tcg aat acg gat gat gaa tta tca gac agc 245
Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser
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Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn
75 80 85

cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa 341
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu
90 95 100

acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag 389
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu
105 110 115

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Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr	
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Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser	
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Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser	
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Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile	
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Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu	
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Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe	
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Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser	
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Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile	
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Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile	
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Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile	
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Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn	
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Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn	Phe	Gly	Asn	Ile	
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gat	tca	cca	tat	att	att	aaa	gtt	att	agt	aaa	tat	gac	cct	aat	aag	1685
Asp	Ser	Pro	Tyr	Ile	Ile	Lys	Val	Ile	Ser	Lys	Tyr	Asp	Pro	Asn	Lys	
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Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met	Gln	Thr	Thr	Ile	
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Asn	Glu	Tyr	Thr	Gly	Glu	Phe	Arg	Thr	Ala	Ser	Tyr	Asp	Asn	Thr	Ile	
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Ala	Phe	Ser	Thr	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Asp	Leu	Pro	Pro	Glu	
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Glu	Asp	Gly	Lys	Tyr	Gln	Phe	Asp	Gly	Leu	Lys	Asn	Gly	Leu	Thr	Tyr	
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Lys	Ile	Thr	Phe	Glu	Thr	Pro	Glu	Gly	Tyr	Thr	Pro	Thr	Leu	Lys	His	
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Ser	Gly	Thr	Asn	Pro	Ala	Leu	Asp	Ser	Glu	Gly	Asn	Ser	Val	Trp	Val	
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Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val	
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Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp	
745 750 755	
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Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile	
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Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser	
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Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr	
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Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp	
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955	960
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tct aaa ggc acg tta ctt gga act ctg ttt gca ggt tta gga gcg tta	3269
Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu	
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 Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr
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 Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asp Glu Glu Lys
 65 70 75 80
 Asn Asp Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn
 85 90 95
 Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys
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 Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu
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 Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu
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 Glu Glu Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile

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Val Gln Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala						
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Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn						
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Thr Ile Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln						
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Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu						
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Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu						
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Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln						
	260		265		270	
Leu Ala Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr						
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Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys						
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Ala His Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp						
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Asp Lys Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn						
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Thr Val Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys						
	340		345		350	
Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn						
	355		360		365	
Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn						
	370		375		380	
Ile Lys Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val						
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Pro Asn Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser						

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Ser Val Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn	420	425	430		
Arg Thr Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn	435	440	445		
His Thr Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala	450	455	460		
Lys Glu Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr	465	470	475	480	
Ile Ile Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn	485	490	495		
Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu	500	505	510		
Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val	515	520	525		
Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile	530	535	540		
Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr	545	550	555	560	
Val Thr Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr	565	570	575		
Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly	580	585	590		
Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val	595	600	605		
Trp Glu Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu	610	615	620		
Lys Pro Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr	625	630	635	640	
Ser Lys Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly	645	650	655		
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Val Trp Tyr Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys		
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Gly Ile Ser Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile		
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Ile Ser Thr Thr Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn		
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Leu Asn Ser Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met		
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Thr Gln Thr Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp		
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Leu Gly Asn Ser Ser Asp Lys Ser Thr Lys Asp Lys Leu Pro Asp Thr		
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Gly Ala Asn Glu Asp Tyr Gly Ser Lys Gly Thr Leu Leu Gly Thr Leu		
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Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg		
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Lys Asn Lys Asn		
1090		